

Supplementary Table 1. Distribution of potential “A-to-I (G)” editing events by transcript regions.

Region	HCC448N	HCC448T	HCC473N	HCC473T	HCC510N	HCC510T
CDS¹	3,679	5,035	3,991	4,564	3,551	5,017
Intron	1,147	1,770	1,245	1,559	1,302	1,445
UTR²	5,045	5,803	5,391	5,931	4,430	6,396
Splicing site	611	990	638	950	737	988
Intergenic	1,406	1,734	1,505	1,874	1,185	2,067
Pseudo/ncRNA³	741	962	728	1,039	630	1,010
Total	12,629	16,294	13,498	15,917	11,835	16,923

¹CDS, coding sequence;

²UTR, untranslated region;

³ncRNA, non-coding RNA.